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Cassava mosaic disease in Madagascar: complex epidemiology and evolutionary dynamics of cassava mosaic geminiviruses

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Cassava is the staple food for hundreds of millions of people in Africa but its cultivation is seriously constrained by cassava mosaic disease (CMD) in Madagascar and in Africa in general.
In this study, we first identified the cassava mosaic geminiviruses (CMGs) involved in CMD in Madagascar and their associated epidemiological characteristics from countrywide surveys. Molecular diagnosis of CMGs in Madagascar revealed an unprecedented diversity and co-occurrence of six CMGs. Distinct geographical distributions were observed for the six viruses. While EACMCV and SACMV were widespread, ACMV was more prevalent in the central highlands, and EACMV and EACMKV were prevalent in lowlands and coastal regions. PCR diagnosis revealed that mixed infection (up to four co-infected viruses) occurred in 21% of the samples and were associated with higher symptom severity scores. Pairwise comparisons of virus associations showed that EACMCV was found in mixed infections more often than expected while ACMV and SACMV were mostly found in single infections. Even if the whitefly vector *Bemisia tabaci* was more abundant in lowland and coastal areas, infected cuttings remain the primary source of CMD propagation (95%) in Madagascar.
Secondly, the genetic and spatial structure of CMGs populations was studied and we applied Bayesian phylogeographic modelling to infer the origins of Madagascan CMG populations within the epidemiological context of related populations situated on mainland Africa and other south western Indian Ocean islands. SACMV and ACMV, the two most prevalent viruses, displayed low degrees of genetic diversity and have most likely been introduced to the island only once. By contrast, EACMV-like CMG populations (EACMV, EAMCKV, EACMCV and complex recombinants of these) were more diverse, more spatially structured, and displayed evidence of at least three independent introductions from mainland Africa.
Our study highlights both the complexity of CMD on Madagascar, and the distinct evolutionary and spatial dynamics of the different viral species that collectively are associated with this disease.

Références :

[1] Harimalala M. *et al.*, 2014. Molecular epidemiology of cassava mosaic disease in Madagascar. *Plant Pathology, Online.*
[2] De Bruyn A. *et al.*, 2014. Divergent evolutionary and epidemiological dynamics of cassava mosaic geminiviruses in Madagascar. *BMC Evolutionary Biology, submitted.*